LIM package:none R Documentation

**Description**

This function performs the Line Intercept Method, proposed by Eberhardt (1978). The main objective of this method is to obtain a cover estimate (abundance and/or density) of a determined species in a community using linear transects.

**Usage**

LIM (object, x, base, area, method=”student”)

**Arguments**

object An object of class data.frame, containing in the first column, the perpendicular width of individuals intercepted by the *i* st transect line; and in the second column, the correspondent number (*i*) of the transect line.

x A vector containing the length of line transects.

base An integer indicating the width of the base line from which the transects begin.

area An integer indicating the total study area where lines were traced. If not specified, the study area will be calculated by dividing the average length of all lines and the baseline.

method The method to calculate confidence intervals for abundance and density means. The default is based in a “t student” distribution (method = “student”), but the other option is to use a bootstrap method with 10000 simulations (method = “bootstrap”).

**Value**

A list containing one matrix with species abundance and density for each transect line; and another matrix showing the confidence interval for mean abundance and density, indicating beyond the mean, the percentiles of 5 and 95%.

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**References**

Eberhardt, L. L. 1978. Transect methods for population studies. Journal of Wildlife Management, 42: 1-31.

Krebs, C. J. 1999. Ecological Methodology, 2nd ed. Addison-Wesley Educational Publishers, Inc.

**Example**

# this is an example found in the book of Krebs (1999). Four lines were laid out at random along a 125 m baseline to estimate the willow density on an irregular area bordering a stream. The study area was 6.3 ha.

# values of the intercept distances

width\_1<-c(1.3, 3.1, 0.8, 2.2, 0.4, 1.7, 0.2, 1.5, 1.9, 0.4, 0.1)

width\_2<-c( 1.1, 0.1, 1.8, 2.7, 2.4, 0.7, 0.4, 0.3, 1.4, 0.1, 2.1, 2.3)

width\_3<-c(0.3, 1.7, 2.1, 0.2, 0.2, 0.4, 1.1, 0.3)

width\_4<-c(3.3, 3.0, 1.4, 0.2, 1.7, 1.1, 0.2, 1.9, 0.9)

width<-c(width\_1, width\_2, width\_3, width\_4)

lines<-c(rep(1,length(width\_1)),rep(2, length(width\_2)),

rep(3, length(width\_3)), rep(4, length(width\_4)))

dat<-data.frame(width,lines)

len<-c(438,682,511,387) # length of each transect line

baseline<-125

area<-6.3

# applying the “LIM function”, using a t student distribution to calculate the confidence intervals for mean

LIM(dat,len,baseline,area)

# applying the “LIM function”, using a bootstrap procedure to calculate the confidence intervals for mean

LIM(dat,len,baseline,area,method= "bootstrap")